

# RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.

Application Serial Number: 10/615,723A  
Source: 1Fw/16  
Date Processed by STIC: 11/17/06

# *ENTERED*



IFW16

RAW SEQUENCE LISTING  
PATENT APPLICATION: US/10/615,723A

DATE: 11/17/2006  
TIME: 08:54:09

Input Set : A:\64129SeqList.txt  
Output Set: N:\CRF4\11172006\J615723A.raw

3 <110> APPLICANT: THE GOVERNMENT OF THE UNITED STATES OF AMERICA AS  
4 REPRESENTED BY THE SECRETARY OF THE DEPARTMENT OF HEALTH AND  
5 HUMAN SERVICES  
6 Zoon, Kathryn C.  
7 Hu, Renqiu  
8 Bekisz, Joseph B.  
9 Hayes, Mark P.  
W--> 10 <120> TITLE OF INVENTION: Interferon Alpha Hybrids  
12 <130> FILE REFERENCE: 4239-64129-01  
14 <140> CURRENT APPLICATION NUMBER: US 10/615,723A  
15 <141> CURRENT FILING DATE: 2003-07-08  
17 <150> PRIOR APPLICATION NUMBER: US 09/744,754  
18 <151> PRIOR FILING DATE: 2001-01-24  
20 <150> PRIOR APPLICATION NUMBER: US 60/094,407  
21 <151> PRIOR FILING DATE: 1998-07-28  
23 <150> PRIOR APPLICATION NUMBER: PCT/US99/15284  
24 <151> PRIOR FILING DATE: 1999-07-06  
26 <160> NUMBER OF SEQ ID NOS: 44  
28 <170> SOFTWARE: PatentIn version 3.1  
30 <210> SEQ ID NO: 1  
31 <211> LENGTH: 27  
32 <212> TYPE: DNA  
33 <213> ORGANISM: Artificial Sequence  
35 <220> FEATURE:  
36 <223> OTHER INFORMATION: Synthetic Oligonucleotide  
38 <400> SEQUENCE: 1  
39 tccggatcct gtgatctgcc tcagacc 27  
42 <210> SEQ ID NO: 2  
43 <211> LENGTH: 27  
44 <212> TYPE: DNA  
45 <213> ORGANISM: Artificial Sequence  
47 <220> FEATURE:  
48 <223> OTHER INFORMATION: Synthetic Oligonucleotide  
50 <400> SEQUENCE: 2  
51 agcagatgag tcctttgtgc tgaagag 27  
54 <210> SEQ ID NO: 3  
55 <211> LENGTH: 27  
56 <212> TYPE: DNA  
57 <213> ORGANISM: Artificial Sequence  
59 <220> FEATURE:  
60 <223> OTHER INFORMATION: Synthetic Oligonucleotide  
62 <400> SEQUENCE: 3  
63 ctttcagca caaaggactc atctgct 27

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Input Set : A:\64129SeqList.txt

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66 <210> SEQ ID NO: 4  
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 68 <212> TYPE: DNA  
 69 <213> ORGANISM: Artificial Sequence  
 71 <220> FEATURE:  
 72 <223> OTHER INFORMATION: Synthetic Oligonucleotide  
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 75 gagctcgcat gctcatcatt cttacttct taaact 36  
 78 <210> SEQ ID NO: 5  
 79 <211> LENGTH: 24  
 80 <212> TYPE: DNA  
 81 <213> ORGANISM: Artificial Sequence  
 83 <220> FEATURE:  
 84 <223> OTHER INFORMATION: Synthetic Oligonucleotide  
 86 <400> SEQUENCE: 5  
 87 cacgcaggcc tcgaggcat tcag 24  
 90 <210> SEQ ID NO: 6  
 91 <211> LENGTH: 24  
 92 <212> TYPE: DNA  
 93 <213> ORGANISM: Artificial Sequence  
 95 <220> FEATURE:  
 96 <223> OTHER INFORMATION: Synthetic Oligonucleotide  
 98 <400> SEQUENCE: 6  
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 102 <210> SEQ ID NO: 7  
 103 <211> LENGTH: 36  
 104 <212> TYPE: DNA  
 105 <213> ORGANISM: Artificial Sequence  
 107 <220> FEATURE:  
 108 <223> OTHER INFORMATION: Synthetic Oligonucleotide  
 110 <400> SEQUENCE: 7  
 111 gagctcgcat gctcatcatt cttcctcct taatct 36  
 114 <210> SEQ ID NO: 8  
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 116 <212> TYPE: DNA  
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 122 <220> FEATURE:  
 123 <221> NAME/KEY: CDS  
 124 <222> LOCATION: (1)..(498)  
 127 <400> SEQUENCE: 8  
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 129 Cys Asp Leu Pro Gln Thr His Ser Leu Gly Asn Arg Arg Ala Leu Ile  
 130 1 5 10 15  
 132 ctc ctg gca caa atg gga aga atc tct cct ttc tcc tgc ctg aag gac 96  
 133 Leu Leu Ala Gln Met Gly Arg Ile Ser Pro Phe Ser Cys Leu Lys Asp  
 134 20 25 30  
 136 aga cat gac ttt gga ttc ccc caa gag gag ttt gat ggc aac cag ttc 144

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137	Arg	His	Asp	Phe	Gly	Phe	Pro	Gln	Glu	Glu	Phe	Asp	Gly	Asn	Gln	Phe	
138																	192
140	cag	aag	gct	caa	gcc	atc	tct	gtc	ctc	cat	gag	atg	atc	cag	cag	acc	
141	Gln	Lys	Ala	Gln	Ala	Ile	Ser	Val	Leu	His	Glu	Met	Ile	Gln	Gln	Thr	
142																	
144	ttc	aat	ctc	ttc	agc	aca	aag	gac	tca	tct	gct	gct	tgg	gat	gag	acc	240
145	Phe	Asn	Leu	Phe	Ser	Thr	Lys	Asp	Ser	Ser	Ala	Ala	Trp	Asp	Glu	Thr	
146																	
148	ctc	cta	gac	aaa	ttc	tac	act	gaa	ctc	tac	cag	cag	ctg	aat	gac	ctg	288
149	Leu	Leu	Asp	Lys	Phe	Tyr	Thr	Glu	Leu	Tyr	Gln	Gln	Leu	Asn	Asp	Leu	
150																	
152	gaa	gcc	tgt	gtg	ata	cag	ggg	gtg	ggg	gtg	aca	gag	act	ccc	ctg	atg	336
153	Glu	Ala	Cys	Val	Ile	Gln	Gly	Val	Gly	Val	Thr	Glu	Thr	Pro	Leu	Met	
154																	
156	aag	gag	gac	tcc	att	ctg	gct	gtg	agg	aaa	tac	ttc	caa	aga	atc	act	384
157	Lys	Glu	Asp	Ser	Ile	Leu	Ala	Val	Arg	Lys	Tyr	Phe	Gln	Arg	Ile	Thr	
158																	
160	ctc	tat	ctg	aaa	gag	aag	aaa	tac	agc	cct	tgt	gcc	tgg	gag	gtt	gtc	432
161	Leu	Tyr	Leu	Lys	Glu	Lys	Tyr	Ser	Pro	Cys	Ala	Trp	Glu	Val	Val		
162																	
164	aga	gca	gaa	atc	atg	aga	tct	ttt	tct	ttg	tca	aca	aac	ttg	caa	gaa	480
165	Arg	Ala	Glu	Ile	Met	Arg	Ser	Phe	Ser	Leu	Ser	Thr	Asn	Leu	Gln	Glu	
166																	
168	145	145	145	145	145	145	145	145	145	145	145	145	145	145	145	145	160
169	agt	tta	aga	agt	aag	gaa	tg										500
170	Ser	Leu	Arg	Ser	Lys	Glu											
173	165	165	165	165	165	165	165	165	165	165	165	165	165	165	165	165	
174	<210>	SEQ	ID	NO:	9												
175	<211>	LENGTH:	166														
176	<212>	TYPE:	PRT														
177	<213>	ORGANISM:	Artificial Sequence														
178	<220>	FEATURE:															
179	<223>	OTHER INFORMATION:	Gene Fusion														
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184	1																15
187	Leu	Leu	Ala	Gln	Met	Gly	Arg	Ile	Ser	Pro	Phe	Ser	Cys	Leu	Lys	Asp	
188																	30
191	Arg	His	Asp	Phe	Gly	Phe	Pro	Gln	Glu	Glu	Phe	Asp	Gly	Asn	Gln	Phe	
192																	45
195	Gln	Lys	Ala	Gln	Ala	Ile	Ser	Val	Leu	His	Glu	Met	Ile	Gln	Gln	Thr	
196																	
199	Phe	Asn	Leu	Phe	Ser	Thr	Lys	Asp	Ser	Ser	Ala	Ala	Trp	Asp	Glu	Thr	
200	65																80
203	Leu	Leu	Asp	Lys	Phe	Tyr	Thr	Glu	Leu	Tyr	Gln	Gln	Leu	Asn	Asp	Leu	
204																	
207	Glu	Ala	Cys	Val	Ile	Gln	Gly	Val	Gly	Val	Thr	Glu	Thr	Pro	Leu	Met	
208																	
211	Lys	Glu	Asp	Ser	Ile	Leu	Ala	Val	Arg	Lys	Tyr	Phe	Gln	Arg	Ile	Thr	
212																	

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215 Leu Tyr Leu Lys Glu Lys Lys Tyr Ser Pro Cys Ala Trp Glu Val Val  
 216 130 135 140  
 219 Arg Ala Glu Ile Met Arg Ser Phe Ser Leu Ser Thr Asn Leu Gln Glu  
 220 145 150 155 160  
 223 Ser Leu Arg Ser Lys Glu  
 224 165  
 227 <210> SEQ ID NO: 10  
 228 <211> LENGTH: 500  
 229 <212> TYPE: DNA  
 230 <213> ORGANISM: Artificial Sequence  
 232 <220> FEATURE:  
 233 <223> OTHER INFORMATION: Gene Fusion  
 235 <220> FEATURE:  
 236 <221> NAME/KEY: CDS  
 237 <222> LOCATION: (1)..(498)  
 240 <400> SEQUENCE: 10  
 241 tgt gat ctg cct cag acc cac agc ctg ggt aat agg agg gcc ttg ata 48  
 242 Cys Asp Leu Pro Gln Thr His Ser Leu Gly Asn Arg Arg Ala Leu Ile  
 243 1 5 10 15  
 245 ctc ctg gca caa atg gga aga atc tct cct ttc tcc tgc ctg aag gac 96  
 246 Leu Leu Ala Gln Met Gly Arg Ile Ser Pro Phe Ser Cys Leu Lys Asp  
 247 20 25 30  
 249 aga cat gac ttt gga ttc ccc cag gag gag ttt gat ggc aac cag ttc 144  
 250 Arg His Asp Phe Gly Phe Pro Gln Glu Phe Asp Gly Asn Gln Phe  
 251 35 40 45  
 253 cag aag gct caa gcc atc tct gtc ctc cat gag atg atc cag cag acc 192  
 254 Gln Lys Ala Gln Ala Ile Ser Val Leu His Glu Met Ile Gln Gln Thr  
 255 50 55 60  
 257 ttc aat ctc ttc agc aca aag gac tca tct gct act tgg gaa cag agc 240  
 258 Phe Asn Leu Phe Ser Thr Lys Asp Ser Ser Ala Thr Trp Glu Gln Ser  
 259 65 70 75 80  
 261 ctc cta gaa aaa ttt tcc act gaa ctt aac cag cag ctg aat gac ctc 288  
 262 Leu Leu Glu Lys Phe Ser Thr Glu Leu Asn Gln Glu Leu Asn Asp Leu  
 263 85 90 95  
 265 gag gcc tgt gtg ata cag ggg gtg ggg gtg aca gag act ccc ctg atg 336  
 266 Glu Ala Cys Val Ile Gln Gly Val Gly Val Thr Glu Thr Pro Leu Met  
 267 100 105 110  
 269 aag gag gac tcc att ctg gct gtg agg aaa tac ttc caa aga atc act 384  
 270 Lys Glu Asp Ser Ile Leu Ala Val Arg Lys Tyr Phe Gln Arg Ile Thr  
 271 115 120 125  
 273 ctc tat ctg aaa gag aag aaa tac agc cct tgt gcc tgg gaa gtt gtc 432  
 274 Leu Tyr Leu Lys Glu Lys Lys Tyr Ser Pro Cys Ala Trp Glu Val Val  
 275 130 135 140  
 277 aga gca gaa atc atg aga tct ttt tct ttg tca aca aac ttg caa gaa 480  
 278 Arg Ala Glu Ile Met Arg Ser Phe Ser Leu Ser Thr Asn Leu Gln Glu  
 279 145 150 155 160  
 281 agt tta aga agt aag gaa tg 500  
 282 Ser Leu Arg Ser Lys Glu  
 283 165

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286 <210> SEQ ID NO: 11  
 287 <211> LENGTH: 166  
 288 <212> TYPE: PRT  
 289 <213> ORGANISM: Artificial Sequence  
 291 <220> FEATURE:  
 292 <223> OTHER INFORMATION: Gene Fusion  
 294 <400> SEQUENCE: 11

296 Cys Asp Leu Pro Gln Thr His Ser Leu Gly Asn Arg Arg Ala Leu Ile  
 297 1 5 10 15  
 300 Leu Leu Ala Gln Met Gly Arg Ile Ser Pro Phe Ser Cys Leu Lys Asp  
 301 20 25 30  
 304 Arg His Asp Phe Gly Phe Pro Gln Glu Glu Phe Asp Gly Asn Gln Phe  
 305 35 40 45  
 308 Gln Lys Ala Gln Ala Ile Ser Val Leu His Glu Met Ile Gln Gln Thr  
 309 50 55 60  
 312 Phe Asn Leu Phe Ser Thr Lys Asp Ser Ser Ala Thr Trp Glu Gln Ser  
 313 65 70 75 80  
 316 Leu Leu Glu Lys Phe Ser Thr Glu Leu Asn Gln Gln Leu Asn Asp Leu  
 317 85 90 95  
 320 Glu Ala Cys Val Ile Gln Gly Val Gly Val Thr Glu Thr Pro Leu Met  
 321 100 105 110  
 324 Lys Glu Asp Ser Ile Leu Ala Val Arg Lys Tyr Phe Gln Arg Ile Thr  
 325 115 120 125  
 328 Leu Tyr Leu Lys Glu Lys Lys Tyr Ser Pro Cys Ala Trp Glu Val Val  
 329 130 135 140  
 332 Arg Ala Glu Ile Met Arg Ser Phe Ser Leu Ser Thr Asn Leu Gln Glu  
 333 145 150 155 160  
 336 Ser Leu Arg Ser Lys Glu  
 337 165  
 340 <210> SEQ ID NO: 12  
 341 <211> LENGTH: 497  
 342 <212> TYPE: DNA  
 343 <213> ORGANISM: Artificial Sequence  
 345 <220> FEATURE:  
 346 <223> OTHER INFORMATION: Gene Fusion  
 348 <220> FEATURE:  
 349 <221> NAME/KEY: CDS  
 350 <222> LOCATION: (1)..(495)  
 353 <400> SEQUENCE: 12

354 tgt gat ctg cct cag acc cac agc ctg ggt agc agg agg acc ttg atg 48  
 355 Cys Asp Leu Pro Gln Thr His Ser Leu Gly Ser Arg Arg Thr Leu Met  
 356 1 5 10 15  
 358 ctc ctg gca cag atg agg aga atc tct ctt ttc tcc tgc ttg aag gac 96  
 359 Leu Leu Ala Gln Met Arg Arg Ile Ser Leu Phe Ser Cys Leu Lys Asp  
 360 20 25 30  
 362 aga cgt gac ttt gga ttt ccc cag gag gag ttt ggc aac cag ttc caa 144  
 363 Arg Arg Asp Phe Gly Phe Pro Gln Glu Glu Phe Gly Asn Gln Phe Gln  
 364 35 40 45  
 366 aag gct gaa acc atc cct gtc ctc cat gag atg atc cag cag atc ttc 192

RAW SEQUENCE LISTING ERROR SUMMARY DATE: 11/17/2006  
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**Please Note:**

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:43; Xaa Pos. 5,9  
Seq#:44; Xaa Pos. 5,9

**VERIFICATION SUMMARY**

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L:10 M:283 W: Missing Blank Line separator, <120> field identifier

L:1444 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:43 after pos.:0

L:1469 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:44 after pos.:0